

Package ‘DiallelAnalysisR’

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Type Package

Title Diallel Analysis with R

Version 0.1.1

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Description Performs Diallel Analysis with R using Griffing's and Hayman's approaches. Four different methods (1: Method-I (Parents + F1's + reciprocals); 2: Method-II (Parents and one set of F1's); 3: Method-III (One set of F1's and reciprocals); 4: Method-IV (One set of F1's only)) and two methods (1: Fixed Effects Model; 2: Random Effects Model) can be applied using Griffing's approach.

Depends R (>= 3.1)

Imports ggplot2, stats

License GPL-2

LazyData TRUE

RoxygenNote 5.0.1.9000

NeedsCompilation no

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R topics documented:

Griffing	2
GriffingData1	6
GriffingData2	7
GriffingData3	8
GriffingData4	9
Hayman	10
HaymanData	12

Index	14
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Griffing

*Diallel Analysis using Griffing Approach***Description**

Griffing is used for performing Diallel Analysis using Griffing's Approach.

Usage

```
Griffing(y, Rep, Cross1, Cross2, data, Method, Model)
```

Arguments

y	Numeric Response Vector
Rep	Replicate as factor
Cross1	Cross 1 as factor
Cross2	Cross 2 as factor
data	A data.frame
Method	Method for Diallel Analysis using Griffing's approach. It can take 1, 2, 3, or 4 as argument depending on the method being used. <ol style="list-style-type: none"> 1. Method-I (Parents + F_1's + reciprocals); 2. Method-II (Parents and one set of F_1's); 3. Method-III (One set of F_1's and reciprocals); 4. Method-IV (One set of F_1's only).
Model	Model for Diallel Analysis using Griffing's approach. It can take 1 or 2 as arguments depending on the model being used. <ol style="list-style-type: none"> 1. Fixed Effects Model; 2. Random Effects Model.

Details

Diallel Analysis using Griffing's approach.

Value

Means Means
 ANOVA Analysis of Variance (ANOVA) table
 Genetic.Components Genetic Components
 Effects Effects of Crosses
 StdErr Standard Errors of Crosses

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

[Hayman](#), [GriffingData1](#), [GriffingData2](#), [GriffingData3](#), [GriffingData4](#)

Examples

```
#-----
## Diallel Analysis with Griffing's Approach Method 1 & Model 1
#-----
Griffing1Data1 <-
  Griffing(
    y      = Yield
    , Rep   = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , data  = GriffingData1
    , Method = 1
    , Model = 1
  )
names(Griffing1Data1)
Griffing1Data1
Griffing1Data1Means <- Griffing1Data1$Means
Griffing1Data1ANOVA <- Griffing1Data1$ANOVA
Griffing1Data1Genetic.Components <- Griffing1Data1$Genetic.Components
Griffing1Data1Effects <- Griffing1Data1$Effects
Griffing1Data1StdErr <- as.matrix(Griffing1Data1$StdErr)

#-----
## Diallel Analysis with Griffing's Approach Method 1 & Model 2
#-----
Griffing2Data1 <-
  Griffing(
    y      = Yield
    , Rep   = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , data  = GriffingData1
    , Method = 1
    , Model = 2
  )
names(Griffing2Data1)
Griffing2Data1
Griffing2Data1Means <- Griffing2Data1$Means
Griffing2Data1ANOVA <- Griffing2Data1$ANOVA
```

```
Griffing2Data1Genetic.Components <- Griffing2Data1$Genetic.Components
```

```
#-----
## Diallel Analysis with Griffing's Approach Method 2 & Model 1
#-----
```

```
Griffing1Data2 <-
  Griffing(
    y      = Yield
    , Rep  = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , data  = GriffingData2
    , Method = 2
    , Model = 1
  )
names(Griffing1Data2)
Griffing1Data2
Griffing1Data2Means <- Griffing1Data2$Means
Griffing1Data2ANOVA <- Griffing1Data2$ANOVA
Griffing1Data2Genetic.Components <- Griffing1Data2$Genetic.Components
Griffing1Data2Effects <- Griffing1Data2$Effects
Griffing1Data2StdErr <- as.matrix(Griffing1Data2$StdErr)
```

```
#-----
## Diallel Analysis with Griffing's Approach Method 2 & Model 2
#-----
```

```
Griffing2Data2 <-
  Griffing(
    y      = Yield
    , Rep  = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , data  = GriffingData2
    , Method = 2
    , Model = 2
  )
names(Griffing2Data2)
Griffing2Data2
Griffing2Data2Means <- Griffing2Data2$Means
Griffing2Data2ANOVA <- Griffing2Data2$ANOVA
Griffing2Data2Genetic.Components <- Griffing2Data2$Genetic.Components
```

```
#-----
## Diallel Analysis with Griffing's Approach Method 3 & Model 1
#-----
```

```
Griffing1Data3 <-
  Griffing(
    y      = Yield
    , Rep  = Rep
    , Cross1 = Cross1
```

```

    , Cross2 = Cross2
    , data   = GriffingData3
    , Method = 3
    , Model  = 1
  )
names(Griffing1Data3)
Griffing1Data3
Griffing1Data3Means <- Griffing1Data3$Means
Griffing1Data3ANOVA <- Griffing1Data3$ANOVA
Griffing1Data3Genetic.Components <- Griffing1Data3$Genetic.Components
Griffing1Data3Effects <- Griffing1Data3$Effects
Griffing1Data3StdErr <- as.matrix(Griffing1Data3$StdErr)

#-----
## Diallel Analysis with Griffing's Approach Method 3 & Model 2
#-----
Griffing2Data3 <-
  Griffing(
    y      = Yield
    , Rep   = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , data  = GriffingData3
    , Method = 3
    , Model  = 2
  )
names(Griffing2Data3)
Griffing2Data3
Griffing2Data3Means <- Griffing2Data3$Means
Griffing2Data3ANOVA <- Griffing2Data3$ANOVA
Griffing2Data3Genetic.Components <- Griffing2Data3$Genetic.Components

#-----
## Diallel Analysis with Griffing's Approach Method 4 & Model 1
#-----
Griffing1Data4 <-
  Griffing(
    y      = Yield
    , Rep   = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , data  = GriffingData4
    , Method = 4
    , Model  = 1
  )
names(Griffing1Data4)
Griffing1Data4
Griffing1Data4Means <- Griffing1Data4$Means
Griffing1Data4ANOVA <- Griffing1Data4$ANOVA
Griffing1Data4Genetic.Components <- Griffing1Data4$Genetic.Components
Griffing1Data4Effects <- Griffing1Data4$Effects

```

```

Griffing1Data4StdErr <- as.matrix(Griffing1Data4$StdErr)

#-----
## Diallel Analysis with Griffing's Approach Method 4 & Model 2
#-----
Griffing2Data4 <-
  Griffing(
    y      = Yield
    , Rep  = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , data  = GriffingData4
    , Method = 4
    , Model = 2
  )
names(Griffing2Data4)
Griffing2Data4
Griffing2Data4Means <- Griffing2Data4$Means
Griffing2Data4ANOVA <- Griffing2Data4$ANOVA
Griffing2Data4Genetic.Components <- Griffing2Data4$Genetic.Components

```

GriffingData1

Data for Diallel Analysis using Griffing Approach Method 1

Description

Griffing is used for performing Diallel Analysis using Griffing's Approach.

Usage

```
data(GriffingData1)
```

Format

A data.frame with 256 rows and 4 variables.

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

[Griffing](#), [GriffingData2](#), [GriffingData3](#), [GriffingData4](#)

Examples

```
data(GriffingData1)
```

GriffingData2

Data for Diallel Analysis using Griffing Approach Method 2

Description

Griffing is used for performing Diallel Analysis using Griffing's Approach.

Usage

```
data(GriffingData2)
```

Format

A data.frame with 144 rows and 4 variables.

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

[Griffing](#), [GriffingData1](#), [GriffingData3](#), [GriffingData4](#)

Examples

```
data(GriffingData2)
```

GriffingData3

Data for Diallel Analysis using Griffing Approach Method 3

Description

Griffing is used for performing Diallel Analysis using Griffing's Approach.

Usage

```
data(GriffingData3)
```

Format

A data.frame with 224 rows and 4 variables.

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9**(4), 463–493.
2. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

[Griffing](#), [GriffingData1](#), [GriffingData2](#), [GriffingData4](#)

Examples

```
data(GriffingData3)
```

Description

Griffing is used for performing Diallel Analysis using Griffing's Approach.

Usage

```
data(GriffingData4)
```

Format

A data.frame with 112 rows and 4 variables.

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

[Griffing](#), [GriffingData1](#), [GriffingData2](#), [GriffingData3](#)

Examples

```
data(GriffingData4)
```

Hayman

Diallel Analysis using Hayman Approach

Description

Hayman is used for performing Diallel Analysis using Hayman's Approach.

Usage

```
Hayman(y, Rep, Cross1, Cross2, data)
```

Arguments

y	Numeric Response Vector
Rep	Replicate as factor
Cross1	Cross 1 as factor
Cross2	Cross 2 as factor
data	A data.frame

Details

Diallel Analysis using Haymans's approach.

Value

Means Means
ANOVA Analysis of Variance (ANOVA) table
Genetic.Components Genetic Components
Effects Effects of Crosses
StdErr Standard Errors of Crosses

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. Hayman, B. I. (1954 a) The Theory and Analysis of Diallel Crosses. *Genetics*, **39**, 789–809.
2. Hayman, B. I. (1954 b) The Analysis of Variance of Diallel Tables. *Biometrics*, **10**, 235–244.
3. Hayman, B. I. (1957) Interaction, Heterosis and Diallel Crosses. *Genetics*, **42**, 336–355.
4. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

[Griffing](#), [HaymanData](#)

Examples

```
#-----
## Diallel Analysis with Haymans's Approach
#-----

Hayman1Data <-
  Hayman(
    y      = Yield
    , Rep  = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , data = HaymanData
  )

Hayman1Data
names(Hayman1Data)

Hayman1DataMeans <- Hayman1Data$Means
Hayman1DataANOVA <- Hayman1Data$ANOVA
Hayman1DataWr.Vr.Table <- Hayman1Data$Wr.Vr.Table

Hayman1DataComponents.of.Variation <- Hayman1Data$Components.of.Variation
Hayman1DataOther.Parameters <- Hayman1Data$Other.Parameters
Hayman1DataFr <- Hayman1Data$Fr

#-----
# Wr-Vr Graph
#-----
VOLO <- Hayman1Data$VOLO
In.Value <- Hayman1Data$In.Value
a <- Hayman1Data$a
b <- Hayman1Data$b
Wr.Vr <- Hayman1Data$Wr.Vr.Table

library(ggplot2)
ggplot(data=data.frame(x=c(0, max(In.Value, Wr.Vr$Vr, Wr.Vr$Wr, Wr.Vr$Wrei))), aes(x)) +
  stat_function(fun=function(x) {sqrt(x*VOLO)}, color="blue") +
  geom_hline(yintercept = 0) +
  geom_vline(xintercept = 0) +
  geom_abline(intercept = a, slope = b) +
  geom_abline(intercept = mean(Wr.Vr$Wr)-mean(Wr.Vr$Vr), slope = 1) +
  geom_segment(aes(
    x      = mean(Wr.Vr$Vr)
    , y    = min(0, mean(Wr.Vr$Wr))
    , xend = mean(Wr.Vr$Vr)
    , yend = max(0, mean(Wr.Vr$Wr))
  ))
)
```

```

, color = "green"
) +
geom_segment(aes(
  x      = min(0, mean(Wr.Vr$Vr))
  , y      = mean(Wr.Vr$Wr)
  , xend   = max(0, mean(Wr.Vr$Vr))
  , yend   = mean(Wr.Vr$Wr)
)
, color = "green"
) +
lims(x=c(min(0, Wr.Vr$Vr, Wr.Vr$Wrei), max(Wr.Vr$Vr, Wr.Vr$Wrei)),
     y=c(min(0, Wr.Vr$Wr, Wr.Vr$Wrei), max(Wr.Vr$Wr, Wr.Vr$Wri)))
) +
labs(
  x = expression(V[r])
  , y = expression(W[r])
  , title = expression(paste(W[r]-V[r] , " Graph"))
) +
theme_bw()

```

HaymanData

Data for Diallel Analysis using Hayman's Approach

Description

Griffing is used for performing Diallel Analysis using Hayman's Approach.

Usage

```
data(HaymanData)
```

Format

A data.frame with 256 rows and 4 variables.

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Test

Examples

```
data(HaymanData)
```

Index

*Topic **datasets**

GriffingData1, [6](#)

GriffingData2, [7](#)

GriffingData3, [8](#)

GriffingData4, [9](#)

HaymanData, [12](#)

Griffing, [2](#), [7-9](#), [11](#)

GriffingData1, [3](#), [6](#), [8](#), [9](#)

GriffingData2, [3](#), [7](#), [7](#), [8](#), [9](#)

GriffingData3, [3](#), [7](#), [8](#), [8](#), [9](#)

GriffingData4, [3](#), [7](#), [8](#), [9](#)

Hayman, [3](#), [10](#)

HaymanData, [11](#), [12](#)